

SEQUENCE LISTING

- SubA12
- (1) GENERAL INFORMATION:
- (i) APPLICANT: LI, ET AL.
- (ii) TITLE OF INVENTION: Human Amine Receptor
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
- (B) STREET: 6 BECKER FARM ROAD
- (C) CITY: ROSELAND
- (D) STATE: NEW JERSEY
- (E) COUNTRY: USA
- (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE: Concurrently
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
- (A) APPLICATION NUMBER:
- (B) FILING DATE:

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(viii)

ATTORNEY/AGENT INFORMATION:

- (A) NAME: FERRARO, GREGORY D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-

(ix)

TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2)

INFORMATION FOR SEQ ID NO:1:

(i)

SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1380 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii)

MOLECULE TYPE: cDNA

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CTAGAGCTAG CAGGAGTAAC TCTCATGGAA COTTGGAAAC CATTCTTCAA TTGAATTTCA 60
GGGCACATTT GAATCAGTAC CCAGGGGCAC TGTACTATGC TCCCAGCTGG ACCTTAGTTT 120
CCTCCTCCTC GTTTCACCCT GTGAGTAATT AACAGACAAA ATTTTTTTTTT TTTTTTTTTT 180
TTTTTTTTTT TTTTGGCCCT CCAGTGGAGA AGGTGGCCAG TTCTCAGACA GAGGAAGAGT 240
AGAAATCATA A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT 290
      - Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro

GCG GCA TTC TGC TAC CAG GTG AAT GGG TCT TGC CCC AGG ACA GTA CAT 338
Ala Ala Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His

ACT CTG GGC ATC CAG TTG GTC ATC TAC CTG ACC TGT GCA GCA GGC ATG 386
Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met

CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC 434
Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr

TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC 482
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SWA12

Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala	
CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT	530
Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile	
CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG	578
Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu	
CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC	626
His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu	
TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC	674
Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu	
TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA	722
Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala	
GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT	770
Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp	
GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG	818
Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val	
GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC	866
Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe	
CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG	914
Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys	
ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC	962
Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser	
AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG AGA AAA GCT GCC AAG ACC	1010
Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr	
CTG GGC ATT GTT GTG GGC ATA TAC CTC TTG TGC TGG CTG CCC TTC ACC	1058
Leu Gly Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr	
ATA GAC ACG ATG GTC GAC AGC CTC CTT CAC TTT ATC ACA CCC CCA CTG	1106
Ile Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu	
GTC TTT GAC ATC TTT ATC TGG TTT GCT TAC TTC AAC TCA GCC TGC AAC	1154
Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn	

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CCC ATC ATC TAT GTC TTT TCC TAC CAG TGG TTT CGG AAG GCA CTG AAA	1202
Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys	
CTC ACA CTG AGC CAG AAG GTC TTC TCA CCG CAG ACA CGC ACT GTT GAT	1250
Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp	
TTG TAC CAA GAA TGATTCCTTC TACTAAATGC AGGCAAGGAG TAGGACCTCA	1302
Leu Tyr Gln Glu	
CAGGAAAGAT AAGTGGCACT GTGACCGCGG GCTGTGTGGT GTTGAGTTTG TGGGCATGCT	1362
TCCAGGACAG CATGGGTT	1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 337 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) STRANDEDNESS:

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro Ala Ala		
5	10	15
Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His Thr		
20	25	30
Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met		
35	40	45
Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser		
50	55	60
Tyr Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser		
65	70	75
Leu Ala Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu		
80	85	90

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Ser Thr Ile Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe	95	100	105
Leu Cys Arg Leu His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr	110	115	120
Ser Ile Phe His Leu Cys Phe Ile Ser Ile Asp Arg His Cys Ala	125	130	135
Ile Cys Asp Pro Leu Leu Tyr Pro Ser Lys Phe Thr Val Arg Val	140	145	150
Ala Leu Arg Tyr Ile Leu Ala Gly Trp Gly Val Pro Ala Ala Tyr	155	160	165
Thr Ser Leu Phe Leu Tyr Thr Asp Val Val Glu Thr Arg Leu Ser	170	175	180
Gln Trp Leu Glu Glu Met Pro Cys Val Gly Ser Cys Gln Leu Leu	185	190	195
Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe Pro Leu Phe Phe Val	200	205	210
Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys Ile Phe Val Val	215	220	225
Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser Lys Ser Leu	230	235	240
Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr Leu Gly	245	250	255
Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr Ile	260	265	270
Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu	275	280	285
Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys	290	295	300
Asn Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala	305	310	315
Leu Lys Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg	320	325	330
Thr Val Asp Leu Tyr Gln Glu	335		